

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,109

DATE: 05/29/2001

TIME: 15:37:28

Input Set : A:\SeqListing.APP.txt

Output Set: C:\CRF3\05292001\I674109.raw

3 <110> APPLICANT: HOECHST MARION ROUSSEL
 5 <120> TITLE OF INVENTION: METHOD FOR SCREENING ANTIMYCOTIC SUBSTANCES USING
 6 ESSENTIAL GENES FROM S.CEREVISIAE
 8 <130> FILE REFERENCE: 16363PC RUU 7
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/674,109
 C--> 11 <141> CURRENT FILING DATE: 2000-11-22
 13 <150> PRIOR APPLICATION NUMBER: 98402254.1
 14 <151> PRIOR FILING DATE: 1998-09-11
 16 <150> PRIOR APPLICATION NUMBER: 98401007.4
 17 <151> PRIOR FILING DATE: 1998-04-24
 E--> 19 <160> NUMBER OF SEQ ID NOS: 180
 21 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

1337 <210> SEQ ID NO: 106
 1338 <211> LENGTH: 62
 1339 <212> TYPE: DNA
 1340 <213> ORGANISM: Artificial Sequence
 1342 <220> FEATURE:
 1343 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
 1344 YML049c-S1
 1346 <400> SEQUENCE: 106
 E--> 1347 aattcctgct cattcaagga aagtctcagg aaattttcac cagctgaagc ttcgtacgc 59
 1474 <210> SEQ ID NO: 117
 1475 <211> LENGTH: 59
 1476 <212> TYPE: DNA
 1477 <213> ORGANISM: Artificial Sequence
 1479 <220> FEATURE:
 1480 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
 1481 YMR211w-S2
 1483 <400> SEQUENCE: 117
 1484 atttcaatca tcttactccg tgaatcaggt tcggaatgat gcataggcca ctagtggatc 60
 E--> 1485 tg 62
 2265 <210> SEQ ID NO: 180
 2266 <211> LENGTH: 62
 2267 <212> TYPE: DNA
 2268 <213> ORGANISM: Artificial Sequence
 2270 <220> FEATURE:
 2271 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
 2272 YPR137w-S2
 2274 <400> SEQUENCE: 180
 2275 aaaagcctgt ttggtcaatg acagctgaat atataccatt gcataggcca ctagtggatc 60
 2276 tg 62
 W--> 2279 imer
 E--> 2280 ymr290c-s1

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~~W--> 2282 <210> SEQ ID NO:
W--> 2282 <211> LENGTH:
W--> 2282 <212> TYPE:
W--> 2282 <213> ORGANISM:
E--> 2282 <400> SEQUENCE: 105
2283 tgagttttac gtccttttgg atttggcgtt tttccactgg cagctgaagc ttcgtacgc 59
2285 <210> SEQ ID NO: 106
2286 <211> LENGTH: 62
2287 <212> TYPE: DNA
2288 <213> ORGANISM: Artificial Sequence
2290 <220> FEATURE:
2291 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
2292 YML049c-S1
2294 <400> SEQUENCE: 106
E--> 2295 aattcctgct cattcaagga aagtctcagg aaattttcac cagctgaagc ttcgtacgc 59
2422 <210> SEQ ID NO: 117
2423 <211> LENGTH: 59
2424 <212> TYPE: DNA
2425 <213> ORGANISM: Artificial Sequence
2427 <220> FEATURE:
2428 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
2429 YMR211w-S2
2431 <400> SEQUENCE: 117
2432 atttcaatca tcttactcgg tgaatcagg tgggaatgat gcataggcca ctagtggatc 60
E--> 2433 tg 62~~

↑
*Disregard, these are errors due
to the duplication of sequences 105-
to 153 as shown on p. 3.*

<210> 180 → Seq. 180 - listed as last on the file.
 <211> 62
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer
 YPR137w-S2

<400> 180
 aaaagcctgt ttggtcaatg acagctgaat atataccatt gcataggcca ctagtggatc 60
 tg

After sequence 180, the listing starts
 over at sequence # 105 and goes to
 sequence # 153. All of this duplication
 must be deleted from the file.

delete

~~YMR290c-S1~~

<400> 105
 tgagttttac gtcttttggg atttggcgtt tttccactgg cagctgaagc ttcgtacgc 59

<210> 106
 <211> 62
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer
 YML049c-S1

<400> 106
 aattcctgct cattcaagga aagtctcagg aaattttcac cagctgaagc ttcgtacgc 59

<210> 107
 <211> 62
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer
 YMR290c-S2

<400> 107

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/674,109

DATE: 05/29/2001

TIME: 15:37:30

Input Set : A:\SeqListing.APP.txt

Output Set: C:\CRF3\05292001\I674109.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1347 M:252 E: No. of Seq. differs, <211>LENGTH:Input:62 Found:59 SEQ:106
L:1485 M:252 E: No. of Seq. differs, <211>LENGTH:Input:59 Found:62 SEQ:117
L:2279 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:2280 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:180
L:2280 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:68 SEQ:180
L:2280 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:2280 M:112 C: (48) String data converted to lower case,
L:2280 M:252 E: No. of Seq. differs, <211>LENGTH:Input:62 Found:68 SEQ:180
L:2282 M:282 W: Numeric Field Identifier Missing, <210> is required.
L:2282 M:282 W: Numeric Field Identifier Missing, <211> is required.
L:2282 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:2282 M:282 W: Numeric Field Identifier Missing, <213> is required.
L:2282 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:180 differs:105
L:2295 M:252 E: No. of Seq. differs, <211>LENGTH:Input:62 Found:59 SEQ:106
L:2433 M:252 E: No. of Seq. differs, <211>LENGTH:Input:59 Found:62 SEQ:117
L:19 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (180) Counted (228)